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Key indicators

Single-crystal X-ray study T = 123 KMean $\sigma(C-C) = 0.003 \text{ Å}$ R factor = 0.041 wR factor = 0.101 Data-to-parameter ratio = 12.5

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The structure of sodium *p*-nitrophenolate tetrahydrate, $Na^+ \cdot C_6H_4NO_3^- \cdot 4H_2O_3$, is presented. The nature of the hydrogen and coordination bonds in this structure is discussed and compared with that of sodium *p*-nitrophenolate dihydrate.

Sodium p-nitrophenolate tetrahydrate

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Comment

The influence of solvents on crystallization in the formation of new structures of organic compounds is well known and this effect can pose serious problems when crystallizing materials for non-linear optical (NLO) applications. Minemoto et al. (1994) have reported problems associated with the selection of solvents for growing crystals of sodium p-nitrophenolate dihydrate (NPNa·2H₂O), a recent NLO material. This orthorhombic dihydrate system (Minemoto et al., 1992) was formed when crystallized from methanol solution, whereas the water solvent gave transparent crystals in solution, but these lost their transparency on exposure to air. We have carried out further investigations on the growth of NPNa with water as solvent. During the course of this study, we found two types of crystals, viz. monoclinic tetrahydrate and monoclinic monohydrate, which are easily distinguishable by their colour, the former being yellow and the latter being red-brown. Some mention of the tetrahydrate form has already been made in a previous report (Brahadeeswaran et al., 1998). The present study reports the structure of this tetrahydrate form, (I), in more detail.



In the tetrahydrate form, we have observed extensive hydrogen bonding. Both O1A and O1B of the nitrophenoxy ions in the asymmetric unit shown in Fig. 1 are hydrogen bonded to four O atoms of the solvate water molecules. The O atoms of the NO₂ group also form hydrogen bonds with water molecules (Table 1). The availability of relatively more water molecules, as well as Na⁺ ions in special positions in this form (see Fig. 2), alters the hydrogen-bonding patterns, compared to the well studied dihydrate form, in which the water molecule is hydrogen bonded only to atom O1 of the nitro-

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The asymmetric unit of the title compound, showing 50% probability displacement ellipsoids. [Please provide revised figure with labels shifted off the ellipsoids.]



Figure 2

Packing diagram of the crystal structure of the title compound.

phenolate (Minemoto *et al.*, 1992). While the Na atom in the tetrahydrate structure forms regular coordination bonds with six neighbouring OW atoms, resulting in octahedral stacking along the crystallographic *a* axis, the Na⁺ cation in the dihy-

drate form interacts only with atom O2 of the NO_2 group and atoms O3 and OW.

Experimental

The title compound was synthesized from equimolar solutions of pnitrophenolate and sodium hydroxide in water. Single crystals of the tetrahydrate form were grown from aqueous solution by solvent evaporation at 300 K. These crystals were found to nucleate and grow to suitable size for examination after 1 d of solution preparation.

Crystal data

Na ⁺ ·C ₆ H ₄ NO ₃ ⁻ ·4H ₂ O	D_m measured by flotation in CHBr ₃ /
$M_r = 233.16$	C ₆ H ₅ CH ₃
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
a = 11.844 (2) Å	Cell parameters from 25
b = 6.8736 (12) Å	reflections
c = 25.939 (6) Å	$\theta = 12.0 - 15.1^{\circ}$
$\beta = 101.038 (17)^{\circ}$	$\mu = 0.17 \text{ mm}^{-1}$
$V = 2072.6 (7) \text{ Å}^3$	T = 123 (2) K
Z = 8	Block, yellow
$D_x = 1.49 \text{ Mg m}^{-3}$	$0.3 \times 0.2 \times 0.2$ mm
$D_m = 1.44 \text{ Mg m}^{-3}$	

 $\theta_{\rm max} = 27.5^{\circ}$

 $h = 0 \rightarrow 15$

 $k = 0 \rightarrow 8$

 $l = -33 \rightarrow 31$

3 standard reflections

every 150 reflections

Data collection

Rigaku AFC-7*S* four-circle diffractometer ω scans 5184 measured reflections 4641 independent reflections 4267 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.016$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.041$ $wR(F^2) = 0.101$ S = 1.124641 reflections 370 parameters All H-atom parameters refined

intensity decay: 4.0% $$\begin{split} &w = 1/[\sigma^2(F_o^{\ 2}) + (0.0304P)^2 \\ &+ 2.0621P] \\ &\text{where } P = (F_o^{\ 2} + 2F_c^{\ 2})/3 \\ (\Delta/\sigma)_{\text{max}} = 0.001 \\ \Delta\rho_{\text{max}} = 0.27 \text{ e } \text{ Å}^{-3} \\ \Delta\rho_{\text{min}} = -0.22 \text{ e } \text{ Å}^{-3} \end{split}$$

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
O3W−H9···O1A ⁱ	0.84 (3)	2.00 (3)	2.828 (2)	166 (3)
$O3W-H10\cdots O1B^{i}$	0.85 (3)	1.93 (3)	2.765 (2)	168 (2)
$O5W-H11\cdots O8W$	0.86 (3)	1.92 (3)	2.769 (2)	170 (3)
O5W−H12···O3A ⁱⁱ	0.80 (3)	2.12 (3)	2.916 (2)	171 (3)
$O7W-H13\cdots O1B^{i}$	0.82(3)	1.97 (3)	2.781 (2)	167 (2)
$O1W-H14\cdots O6W$	0.86 (3)	1.93 (3)	2.763 (2)	164 (2)
$O6W-H15\cdots O2B^{ii}$	0.86 (3)	2.11 (3)	2.924 (2)	158 (3)
$O2W-H16\cdots O1A^{iii}$	0.86 (3)	2.00 (3)	2.857 (2)	176 (3)
$O7W - H17 \cdot \cdot \cdot O3B^{iv}$	0.85 (3)	2.05 (3)	2.891 (2)	170 (2)
$O6W - H18 \cdots O1W^{v}$	0.83 (3)	1.96 (3)	2.778 (2)	166 (3)
$O1W-H19\cdots O1B^{vi}$	0.81(3)	2.01(3)	2.753 (2)	153 (3)
$O2W-H20\cdots O2A^{ii}$	0.82(3)	2.10(3)	2.908 (2)	170 (3)
$O8W-H21\cdots O1A$	0.79 (3)	2.01(3)	2.781 (2)	164 (3)
$O8W - H22 \cdot \cdot \cdot O4W^{vii}$	0.81(3)	1.99 (3)	2.791 (2)	171 (3)
$O4W-H23\cdots O1A^{i}$	0.91 (3)	1.85 (3)	2.744 (2)	171 (2)
$O4W-H24\cdots O1B^{viii}$	0.83 (3)	2.04 (3)	2.856 (2)	168 (3)

Symmetry constants: (i) 1 - x, 2 - y, -z; (ii) 1 - x, y - z, z - z; (iii) x, y - 1, z; (iv) $x - 1, \frac{2}{2} - y, z - \frac{1}{2};$ (v) -x, 1 - y, -z; (vi) x - 1, y, z; (vii) x, 1 + y, z; (viii) 1 - x, 1 - y, -z.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1985); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *TEXSAN* (Molecular Structure Corporation, 1993); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine

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structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *INSIGHT*II (Biosym Technologies, 1995) and *Xtal_GX* (Hall & du Boulay, 1995); software used to prepare material for publication: *WinGX* publication routines (Farrugia, 1999).

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